

- 1 -

piece 1, NC_000913, atpI_gidB+, config: linear, direction: +, begin: 3920434, end: 3921099

5' a c g t t c g a c t c a c a g a c a c a g a c a t c a c t t t c a c t c t c g t c c t t c a g g g t a t g c c g c g t g t c g t a t a a a c 3'

* * 3920440 * * 3920450 * * 3920460 * * 3920470 * * 3920480 * * 3920490 * * 3920500 * * 3920510

- asn - val - ser - thr - his - glu - arg - his - arg - his - val - phe - his - ser - cys - ser - leu - arg - gly - met - pro - arg - val - val - .

- thr - phe - arg - leu - thr - ser - asp - thr - asp - ile - thr - phe - phe - thr - pro - ala - pro - phe - glu - val - cys - arg - val - ser - tyr - lys - thr -

- arg - phe - asp - ser - arg - ala - thr - gln - thr - ser - arg - phe - ser - leu - leu - leu - pro - ser - arg - tyr - ala - ala - cys - arg - ile - lys - thr -

...] NC_000913.ap1

The diagram illustrates a genetic sequence with the following features:

- sd**: A start site (green box) located at position 3920573.
- ir**: An inverted repeat (yellow box) located between positions 3920573 and 3920575.
- orf**: An open reading frame (red box) spanning from position 3920575 to 3920581, consisting of 7 codons.
- atpI_gidB+**: A gene name located at position 3920573.
- total**: The total length of the sequence shown is 5.5 bits.
- ... sd**: Ellipses indicating the sequence continues, ending with another start site (sd).

The diagram shows the 3' end of the 3920670 mRNA sequence. The sequence starts with an fMet codon (AUG) at position 1. The reading frame then continues through the sequence, with each codon's corresponding amino acid color-coded: fMet (red), phe (green), lys (blue), lys (blue), tyr (orange), phe (green), ser (red), ser (red), ala (green), tyr (orange), asn (red), cys (blue), asp (green), phe (green), ser (red), ala (green), asn (red), pro (green), val (green), arg (blue), ser (red), leu (green), glu (red), lys (blue), leu (green). The sequence ends at position 600.

{-----} sd-(8)-ir 3920609 Gap 2.4 bits

[###> orf 21 codons

A diagram of a memory cell. It features a central vertical rectangle representing the floating gate, which is partially shaded green. Above it is a larger, light blue shaded area representing the control gate. Red arrows point from the text "p10 2.1 bits" to both the floating gate and the control gate.

sd-ir_3920609 atpI_gidB+ total 12.2 bits

sd

p35 5.6 bits

} p35-(21)-p10 3920634 Gap 3.3 bits

p35-p10 3920634 total 9.2 bits

 p35 5.2 bits

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-----} p35-(23)-p10 3920646 Gap 1.4 bits  
-----} p35-p10 3920646 total 5.8 bits
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The diagram illustrates the 3920680-3920750 gene cluster. It shows the DNA sequence (5' to 3') with transcription start sites indicated by asterisks (*). The genes are color-coded: 3920680 (red), 3920690 (green), 3920700 (blue), 3920710 (orange), 3920720 (purple), 3920730 (pink), 3920740 (yellow), and 3920750 (light blue). Promoters are shown as dashed lines above the genes. Amino acid sequences are listed below the genes, with cysteine (cys) and lysine (lys) residues highlighted in red circles. The sequence ends with a stop codon (threonyl-tRNA synthetase, Tyr).

... sd

... p35
... p35
... p35



